

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/717,665 A

Source: 1 FWO

Date Processed by STIC: 1/27/05

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 01/27/2005

PATENT APPLICATION: US/10/717,665A

TIME: 10:25:57

Input Set : A:\sequence listing -10717665.txt

Output Set: N:\CRF4\01272005\J717665A.raw

3 <110> APPLICANT: OriGene Technologies, Inc  
 5 <120> TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides  
 7 <130> FILE REFERENCE: 1U 103 R1  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/717,665A  
 C--> 9 <141> CURRENT FILING DATE: 2003-11-21  
 9 <160> NUMBER OF SEQ ID NOS: 80  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 5682  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Homo sapiens  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (62)..(1195)  
 21 <223> OTHER INFORMATION:  
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 25 ccgcctcttc ctctcgggcc catattgaac tcgagttgga agaggcgagt ccggtctcaa 60  
 27 a atg gag gta aaa ccg ccg ccc ggt cgc ccc cag ccc gac tcc ggc cgt 109  
 28 Met Glu Val Lys Pro Pro Pro Gly Arg Pro Gln Pro Asp Ser Gly Arg  
 29 1 5 10 15  
 31 cgc cgt cgc cgc cgg ggg gag gag ggc cat gat cca aag gaa cca gag 157  
 32 Arg Arg Arg Arg Arg Gly Glu Glu Gly His Asp Pro Lys Glu Pro Glu  
 33 20 25 30  
 35 cag ttg aga aaa ctg ttt att ggt ggt ctg agc ttt gaa act aca gat 205  
 36 Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu Thr Thr Asp  
 37 35 40 45  
 39 gat agt tta cga gaa cat ttt gag aaa tgg ggc aca ctc aca gat tgt 253  
 40 Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly Thr Leu Thr Asp Cys  
 41 50 55 60  
 43 gtg gta atg aga gac ccc caa aca aaa cgt tcc agg ggc ttt ggt ttt 301  
 44 Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly Phe Gly Phe  
 45 65 70 75 80  
 47 gtg act tat tct tgt gtt gaa gag gtg gat gca gca atg tgt gct cga 349  
 48 Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala Ala Met Cys Ala Arg  
 49 85 90 95  
 51 cca cac aag gtt gat ggg cgt gta gtg gaa cca aag aga gct gtt tct 397  
 52 Pro His Lys Val Asp Gly Arg Val Val Glu Pro Lys Arg Ala Val Ser  
 53 100 105 110  
 55 aga gag gat tct gta aag cct ggt gcc cat cta aca gtg aag aaa att 445  
 56 Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu Thr Val Lys Lys Ile  
 57 115 120 125  
 59 ttt gtt ggt ggt att aaa gaa gat aca gaa gaa tat aat ttg aga gac 493  
 60 Phe Val Gly Gly Ile Lys Glu Asp Thr Glu Glu Tyr Asn Leu Arg Asp

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61	130	135	140	
63	tac ttt gaa aag tat ggc aag att gaa acc ata gaa gtt atg gaa gac	541		
64	Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile Glu Val Met Glu Asp			
65	145 150 155 160			
67	agg cag agt gga aaa aag aga gga ttt gct ttt gta act ttt gat gat	589		
68	Arg Gln Ser Gly Lys Lys Arg Gly Phe Ala Phe Val Thr Phe Asp Asp			
69	165 170 175			
71	cat gat aca gtt gat aaa att gtt gtt cag aaa tac cac act att aat	637		
72	His Asp Thr Val Asp Lys Ile Val Val Gln Lys Tyr His Thr Ile Asn			
73	180 185 190			
75	ggg cat aat tgt gaa gtg aaa aag gcc ctt tct aaa caa gag atg cag	685		
76	Gly His Asn Cys Glu Val Lys Lys Ala Leu Ser Lys Gln Glu Met Gln			
77	195 200 205			
79	tct gct gga tca cag aga ggt cgt gga ggt gga tct ggc aat ttt atg	733		
80	Ser Ala Gly Ser Gln Arg Gly Arg Gly Gly Gly Ser Gly Asn Phe Met			
81	210 215 220			
83	ggt cgc gga ggg aac ttt gga ggt ggt gga ggt aat ttt ggc cgt ggt	781		
84	Gly Arg Gly Gly Asn Phe Gly Gly Gly Gly Gly Asn Phe Gly Arg Gly			
85	225 230 235 240			
87	gga aac ttt ggt gga aga gga ggc tat ggt ggt gga ggt ggt ggc agc	829		
88	Gly Asn Phe Gly Gly Arg Gly Gly Tyr Gly Gly Gly Gly Gly Gly Ser			
89	245 250 255			
91	aga ggt agt tat gga gga ggt gat ggt gga tat aat gga ttt gga ggt	877		
92	Arg Gly Ser Tyr Gly Gly Gly Asp Gly Gly Tyr Asn Gly Phe Gly Gly			
93	260 265 270			
95	gat ggt ggc aac tat ggc ggt ggt cct ggt tat agt agt aga ggg ggc	925		
96	Asp Gly Gly Asn Tyr Gly Gly Gly Pro Gly Tyr Ser Ser Arg Gly Gly			
97	275 280 285			
99	tat ggt ggt ggt gga cca gga tat gga aac caa ggt ggt gga tat ggt	973		
100	Tyr Gly Gly Gly Gly Pro Gly Tyr Gly Asn Gln Gly Gly Gly Tyr Gly			
101	290 295 300			
103	gga ggt gga gga tat gat ggt tac aat gaa gga gga aat ttt ggc ggt	1021		
104	Gly Gly Gly Gly Tyr Asp Gly Tyr Asn Glu Gly Gly Asn Phe Gly Gly			
105	305 310 315 320			
107	ggt aac tat ggt ggt ggt ggg aac tat aat gat ttt gga aat tat agt	1069		
108	Gly Asn Tyr Gly Gly Gly Gly Asn Tyr Asn Asp Phe Gly Asn Tyr Ser			
109	325 330 335			
111	gga caa cag caa tca aat tat gga ccc atg aaa ggg ggc agt ttt ggt	1117		
112	Gly Gln Gln Gln Ser Asn Tyr Gly Pro Met Lys Gly Gly Ser Phe Gly			
113	340 345 350			
115	gga aga agc tcg ggc agt ccc tat ggt ggt ggt tat gga tct ggt ggt	1165		
116	Gly Arg Ser Ser Gly Ser Pro Tyr Gly Gly Gly Tyr Gly Ser Gly Gly			
117	355 360 365			
119	gga agt ggt gga tat ggt agc aga agg ttc taaaaacagc agaaaagggc	1215		
120	Gly Ser Gly Gly Tyr Gly Ser Arg Arg Phe			
121	370 375			
123	tacagttctt agcaggagag agagcgagga gttgtcagga aagctgcagg ttactttgag	1275		
125	acagtcgtcc caaatgcatt agaggaactg taaaaatctg ccacagaagg aacgatgac	1335		
127	catagtcaga aaagttactg cagcttaaac aggaaaccct tcttgttcag gactgtcata	1395		

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129	gccacagttt	gcaaaaaagt	gagctattga	ttaatgcaat	gtagtgtaa	ttagatgtac	1455
131	attcctgagg	tcttttatct	gtttagactt	tgtctttttc	tttttctttt	cattacatca	1515
133	ggtatattgc	cctgtaaatt	gtgtagtg	taccaggaat	aaaaaattaa	ggaattttta	1575
135	acttttcaat	atttgtgtag	ttcagttttt	ctacatttta	gtacagaaac	tttaacaaaa	1635
137	tgcagtttcg	aaggtgtttc	cttgtgagtt	aacaagtaaa	gaagatcatt	gttaattact	1695
139	attttgtatg	aattttgcta	aagttaaactg	taaagaaaca	cctgctgact	tgcagtttaa	1755
141	ggggaatcta	ttctcccat	ttccaaacca	tgatatgaat	gggcgtgac	atgtggagag	1815
143	aatagataat	ttgtgtgttt	gcaatgtgtg	ttttagataa	ataggattgg	gtattttaat	1875
145	tagcatttgt	gaatttaata	gcattaagat	taccttcaaa	tgaaaaaaa	tctcaaaatt	1935
147	tctatttgtt	ttttgtgcat	tttcttttaa	aatgtaata	tatgatttta	gtgtgttaga	1995
149	cttgctgagt	cctagctgtg	tttagaacat	ctctattcta	catttacctt	ggtaaaattt	2055
151	gaactgctgc	cataggtttt	gggtgtaaag	aatgtttact	gccctccatt	ttaaattctga	2115
153	aaagggatgg	tggatgtttt	ccctctccta	cgttagaaac	cattcttaaa	aacttttgaa	2175
155	aataatagaac	cattaagcct	gctatatctg	agcaaatata	tgggtacctt	ttttttctta	2235
157	ttttaagcac	aagaggccca	taaatcttga	gttactttta	attctttttt	ttgatacaag	2295
159	ttttcagagc	aagagaataa	aaatcatgtg	ttattaaacc	cctaactggc	tggcatgctt	2355
161	tctgttttgt	attctataca	ttttgctgga	tgaaccaag	gatagttcag	gtataattgt	2415
163	ccaaaataac	ctaactgcag	cagaaatgta	gcacagttgc	ttagtacagg	cttctcactt	2475
165	cctacagacc	tgaattcaaa	tttgatagtg	ctgagttctt	aaattcccaa	agaacacact	2535
167	gttatttctt	gtgtatat	caacataaat	catgttggtt	ccaatttggt	tgggaaggccc	2595
169	tgggtgagaa	gagtttttagt	taataagggtc	atatatacat	atattaatat	aaaccaatgt	2655
171	ctactgtttt	gctccagcta	gtgcttacag	tttcattcga	gccctgagta	tgtgccctgc	2715
173	tgttactctc	tttggtagtt	gaacgttgaa	ttcaagtctt	ttgttttaag	aagtactaag	2775
175	caaacaagca	ataaaaagg	gaatggggtg	tgctagtgtt	tgaatatgct	ctctgtgtgc	2835
177	tctaattctg	tgcctctgtg	cattaatatt	tggatgcatg	caatgccagc	atggaaattg	2895
179	gtcttcacat	atactgcagt	tttccagaaa	cattcacaaa	ccaataaatg	taacagacat	2955
181	tccatttgtt	aatgggcata	tatgtgaaaa	gcagtgtaga	aaataggcta	atattagaaa	3015
183	atggttaagt	cctaaataac	ttcaagtgtg	gttatataat	ggacactgtc	aatgttcata	3075
185	acttaaacct	gggtacctgg	tcaaaataat	gcttgggaaa	cattaaaatt	gagctaaatt	3135
187	gtctcaagtt	cttttattca	tataaataaa	gtttaaagga	atgggggaga	ttaacatttc	3195
189	ctgttttatg	tttgtgaaat	tgtttgacac	aaccttgaca	gtatccttta	atggcatgag	3255
191	gttaattgta	ctgttaacca	actttctatg	ttctggaact	agtattatag	tgaaaacatt	3315
193	tacagtaagt	tgatgtttac	aacctataag	cagggtgaaat	ctgtgtatgt	gacctgttta	3375
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197	tttaaccacc	tttaaggac	ctaagatgtg	ctttttaagc	acagtgtgga	tcacagaaac	3495
199	tcactaagac	aggacttcag	cagccttttg	tgtttggaca	agtcagcata	aataaagaat	3555
201	gacaaggcag	cagcaagagc	ttcaactaca	gagaagtga	ggcataagat	actatgatga	3615
203	tagtgagcaa	ctttccaaaa	gctagttaaa	tctgcttatt	acaactgaaa	tatcgaagaa	3675
205	agtctagcag	gaaggagctc	ttcgcccttt	ggaacatcaa	tgagagatag	ttgccacagt	3735
207	cactaggtct	agcatttaga	cctgcaagga	agggcaataa	gcattaggta	aggcttgaat	3795
209	ttgaattttt	tactaatta	aagagtaatt	ttttgtaaag	caaggtaaga	gtaattcttt	3855
211	tgaattgcag	gttgaatgag	aacctacttt	gcctaaatga	ggaatgtctt	tcctaccatc	3915
213	taaaatacga	aggtttctgg	ctgggttaag	ttttagtttg	acagtaaaac	ctgatgacac	3975
215	catttgtttc	cctgcaagtc	tacattacat	atttcacaac	tttgtccctc	tctagtaggc	4035
217	acattggaaa	aattcttcaa	ctgaaaaacta	ccttggtacc	atgtcctaca	cgttttaaac	4095
219	cttagtttta	aaaattcccc	tgcgaaatag	ccataagtat	tcatatcaag	tcagttgtga	4155
221	ctccttggtg	atacaattca	ttttttgtgt	cttcagggtg	aactcaattt	ttggtaaagt	4215
223	ggtttcagct	tttgtgaaaa	ccgtttttgt	gtgtaagcat	gacacacaac	agactcagta	4275
225	agctgcccat	cctcatacta	ggaaaacacc	ttcaaaggaa	cattaaaagt	taccagggcc	4335

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Input Set : A:\sequence listing -10717665.txt

Output Set : N:\CRF4\01272005\J717665A.raw

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227 aggcacagtg gctcacgcct gtaatcccag cactttggga ggctgaggca gatggatccc 4395
229 aagtcaggga atttgagacg agcctgggca acatagttag agcctgtcaa caaaaaatag 4455
231 aaaaattagt tgggcttggt gatacacatc tgtagtccca gctatttggg aggctgcctt 4515
233 gatatcaggc agtcgaggct gcagttagct gactgcccc ctgtattcca gcctgggtga 4575
235 ccccatctca aagaagaaaa gttaccagat gtcatgggta aagggttggtc ttcaagtggc 4635
237 ctcataagtt gtcttgcat taaattcagg gaattcattg gaccaatagg ttacattttc 4695
239 gttccttttt tgttttgggt catctgttaa gcagtggggg cctaattact gtccttttgt 4755
241 aaaaacacat tttcccaaag aacactgaat taccgttcaa actggttggt gatgggtaat 4815
243 aagggtgtgt tttgctgccc caaaagggct taacaattta ggcggatagt ttacttaaaa 4875
245 aaaaaaatcc tttggagaca tactgaaaat gcaactagt ttctaaatta tcaattccct 4935
247 acatgaagaa gcagtttgcc agagtttagt ctcagaaaat gactgggttg ctctatttaa 4995
249 atcagaaccc aatttctacg cgtgttgaat aaggtaacag cctttgatga atttccttca 5055
251 caacatgggt ttagtgaagc aaacattttt tttttaaggg cattgttctt tctagtttat 5115
253 ttctttttat gaaataaaa tattttattt aaacagttcc attgtcgttt ctgaaaacta 5175
255 cagtattctc agaagttgta gcagcagtaa aaaaaaaaaa gttgttatat aagtgattgg 5235
257 ggcagattta actgattttg ttaaaccaat ttgtaagtta ctgcttctaa tattacactt 5295
259 ctaaaaagct gaatttatac tcatgtccta aaggagaata tgtggtaata aagtatatat 5355
261 gttaagtaac taattgaaat aggccttggt ttaagagttc cagtatataa taatcacaaa 5415
263 ttgaaacctg acagtatctt gggagttcca gtaatgtcac aaattagtga ataagcatgc 5475
265 cagtgtgcaa gggtaatgta aggattgtta gcctatctaa atattcaaaa ttactttaaa 5535
267 acttaagtat gttttctgat ttttaagaat tcagaagtgt tctgtaatgg attcagatgt 5595
269 ttcatttgta gtataatgaa atgtttacag aaagataact ttttcattaa aatattttta 5655
271 gaaatgtgaa aaaaaaaaaa aaaaaaa 5682
274 <210> SEQ ID NO: 2
275 <211> LENGTH: 378
276 <212> TYPE: PRT
277 <213> ORGANISM: Homo sapiens
279 <400> SEQUENCE: 2
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282 1 5 10 15
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286 20 25 30
289 Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu Thr Thr Asp
290 35 40 45
293 Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly Thr Leu Thr Asp Cys
294 50 55 60
297 Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly Phe Gly Phe
298 65 70 75 80
301 Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala Ala Met Cys Ala Arg
302 85 90 95
305 Pro His Lys Val Asp Gly Arg Val Val Glu Pro Lys Arg Ala Val Ser
306 100 105 110
309 Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu Thr Val Lys Lys Ile
310 115 120 125
313 Phe Val Gly Gly Ile Lys Glu Asp Thr Glu Glu Tyr Asn Leu Arg Asp
314 130 135 140
317 Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile Glu Val Met Glu Asp
318 145 150 155 160
321 Arg Gln Ser Gly Lys Lys Arg Gly Phe Ala Phe Val Thr Phe Asp Asp

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Input Set : A:\sequence listing -10717665.txt

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322                               165                               170                               175
325 His Asp Thr Val Asp Lys Ile Val Val Gln Lys Tyr His Thr Ile Asn
326                               180                               185                               190
329 Gly His Asn Cys Glu Val Lys Lys Ala Leu Ser Lys Gln Glu Met Gln
330                               195                               200                               205
333 Ser Ala Gly Ser Gln Arg Gly Arg Gly Gly Gly Ser Gly Asn Phe Met
334                               210                               215                               220
337 Gly Arg Gly Gly Asn Phe Gly Gly Gly Gly Gly Asn Phe Gly Arg Gly
338 225                               230                               235                               240
341 Gly Asn Phe Gly Gly Arg Gly Gly Tyr Gly Gly Gly Gly Gly Gly Ser
342                               245                               250                               255
345 Arg Gly Ser Tyr Gly Gly Gly Asp Gly Gly Tyr Asn Gly Phe Gly Gly
346                               260                               265                               270
349 Asp Gly Gly Asn Tyr Gly Gly Gly Pro Gly Tyr Ser Ser Arg Gly Gly
350                               275                               280                               285
353 Tyr Gly Gly Gly Gly Pro Gly Tyr Gly Asn Gln Gly Gly Gly Tyr Gly
354                               290                               295                               300
357 Gly Gly Gly Gly Tyr Asp Gly Tyr Asn Glu Gly Gly Asn Phe Gly Gly
358 305                               310                               315                               320
361 Gly Asn Tyr Gly Gly Gly Gly Asn Tyr Asn Asp Phe Gly Asn Tyr Ser
362                               325                               330                               335
365 Gly Gln Gln Gln Ser Asn Tyr Gly Pro Met Lys Gly Gly Ser Phe Gly
366                               340                               345                               350
369 Gly Arg Ser Ser Gly Ser Pro Tyr Gly Gly Gly Tyr Gly Ser Gly Gly
370                               355                               360                               365
373 Gly Ser Gly Gly Tyr Gly Ser Arg Arg Phe
374                               370                               375

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377 &lt;210&gt; SEQ ID NO: 3

378 &lt;211&gt; LENGTH: 3985

379 &lt;212&gt; TYPE: DNA

380 &lt;213&gt; ORGANISM: Homo sapiens

382 &lt;220&gt; FEATURE:

383 &lt;221&gt; NAME/KEY: CDS

384 &lt;222&gt; LOCATION: (187)..(2529)

385 &lt;223&gt; OTHER INFORMATION:

W--&gt; 388 &lt;400&gt; 3

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389 cttttgggct ggaggctcca ctttttgtgt ttcccgacaca gtcaatcaaa ataggaaaaa 60
391 aaaatccccg gaccgctccg gccgtgtccg ccgcgccttc ccgcatactc tcccgcgcgc 120
393 gccgccttcg ctctcacca tgtgtaaggc ggcggggagc cccgcctgag gtgccctaaa 180
395 cacact atg acc gct ccc gaa aag ccc gtg aaa caa gag gaa atg gct 228
396 Met Thr Ala Pro Glu Lys Pro Val Lys Gln Glu Glu Met Ala
397 1 5 10
399 gcc ttg gac gtg gat agc ggc ggc ggc ggt ggc ggc ggc ggc ggc cac 276
400 Ala Leu Asp Val Asp Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly His
401 15 20 25 30
403 ggc gag tat ctg cag cag cag caa cag cac gga aac ggt gcg gtg gcg 324
404 Gly Glu Tyr Leu Gln Gln Gln Gln Gln His Gly Asn Gly Ala Val Ala
405 35 40 45
407 gcg gca gcg gcg gcc cag gac act cag ccg tca ccg ctc gct ctg ctg 372

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\sequence listing -10717665.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the  
Sequence Listing to ensure that a corresponding explanation is presented in the <220>  
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; Xaa Pos. 162

Seq#:46; Xaa Pos. 162

## VERIFICATION SUMMARY

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Input Set : A:\sequence listing -10717665.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:24 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21  
L:388 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:385  
L:856 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:853  
L:1306 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:1303  
L:1658 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1655  
L:2110 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:2107  
L:2372 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:2369  
L:2572 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:2569  
L:2924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:2921  
L:3558 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:3555  
L:4176 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:4173  
L:4810 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:4807  
L:5502 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:5499  
L:5712 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:5709  
L:6306 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:6303  
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L:7232 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37,Line#:7229  
L:7778 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:7775  
L:8158 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:41,Line#:8155  
L:8304 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:43,Line#:8301  
L:8766 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:45,Line#:8763  
L:8824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:1008  
L:9050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:160  
L:9185 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:47,Line#:9182  
L:9685 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:49,Line#:9682  
L:9857 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:51,Line#:9854  
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L:10991 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:57,Line#:10988